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TECH CENTER 1600, 2900

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/609,543

DATE: 08/15/2001

TIME: 12:32:42

Input Set : A:\Cu57cipl.app

Output Set: N:\CRF3\08152001\I609543.raw

ENTERED

3 <110> APPLICANT: Jeffers, Michael  
 4 Shimkets, Richard A  
 5 Sudhirdas, Prayaga K  
 6 Boldog, Ferenc L  
 7 Yang, Meija  
 8 Burgess, Catherine  
 9 Fernandes, Elma  
 10 Hermann, John L  
 11 LaRochelle, William J  
 12 Lichenstein, Henri  
 14 <120> TITLE OF INVENTION: Novel Fibroblast Growth Factor and Nucleic Acids  
 15 Encoding Same  
 17 <130> FILE REFERENCE: 15966-557 CIP1  
 19 <140> CURRENT APPLICATION NUMBER: 09/609,543  
 20 <141> CURRENT FILING DATE: 2000-07-03  
 22 <150> PRIOR APPLICATION NUMBER: 09/494,585  
 23 <151> PRIOR FILING DATE: 2000-01-31  
 25 <150> PRIOR APPLICATION NUMBER: 60/145,899  
 26 <151> PRIOR FILING DATE: 1999-07-27  
 28 <160> NUMBER OF SEQ ID NOS: 25  
 30 <170> SOFTWARE: PatentIn Ver. 2.1  
 32 <210> SEQ ID NO: 1  
 33 <211> LENGTH: 633  
 34 <212> TYPE: DNA  
 35 <213> ORGANISM: Homo sapiens  
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 40 aggagcgcgg cggagcggag cgcgcgcggc gggccggggg ctgcgcagct ggcgcacctg 180  
 41 cacggcatcc tgcgcgcggc gcagctctat tgcgcaccg gcttcacct gcagatcctg 240  
 42 cccgacggca gcggtcaggg caccggcag gaccacagcc tcttcggtat cttggaattc 300  
 43 atcagtgtgg cagtgggact ggtcagtatt agagggtgtg acagtgggtct ctatcttgga 360  
 44 atgaatgaca aaggagaact ctatggatca gagaaactta cttccgaatg catctttagg 420  
 45 gagcagtttg aagagaactg gtataacacc tattcatcta acatatataa acatggagac 480  
 46 actggccgca ggtattttgt ggcacttaac aaagacgga ctccaagaga tggcgccagg 540  
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 53 <212> TYPE: PRT  
 54 <213> ORGANISM: Homo sapiens  
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 58 1 5 10 15  
 60 Leu Gly Gln Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Gly Glu  
 61 20 25 30  
 63 Arg Pro Pro Leu Leu Gly Glu Arg Arg Ser Ala Ala Glu Arg Ser Ala

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64          35          40          45
66 Arg Gly Gly Pro Gly Ala Ala Gln Leu Ala His Leu His Gly Ile Leu
67          50          55          60
69 Arg Arg Arg Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu
70 65          70          75          80
72 Pro Asp Gly Ser Val Gln Gly Thr Arg Gln Asp His Ser Leu Phe Gly
73          85          90          95
75 Ile Leu Glu Phe Ile Ser Val Ala Val Gly Leu Val Ser Ile Arg Gly
76          100          105          110
78 Val Asp Ser Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Tyr
79          115          120          125
81 Gly Ser Glu Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu
82          130          135          140
84 Glu Asn Trp Tyr Asn Thr Tyr Ser Ser Asn Ile Tyr Lys His Gly Asp
85 145          150          155          160
87 Thr Gly Arg Arg Tyr Phe Val Ala Leu Asn Lys Asp Gly Thr Pro Arg
88          165          170          175
90 Asp Gly Ala Arg Ser Lys Arg His Gln Lys Phe Thr His Phe Leu Pro
91          180          185          190
93 Arg Pro Val Asp Pro Glu Arg Val Pro Glu Leu Tyr Lys Asp Leu Leu
94          195          200          205
96 Met Tyr Thr
97          210
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101 <211> LENGTH: 38
102 <212> TYPE: DNA
103 <213> ORGANISM: Artificial Sequence
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Description of Artificial Sequence:FGF-CX Forward
107     Primer
109 <400> SEQUENCE: 3
110 ctcgtcagat ctccaccatg gctcccttag ccgaagtc 38
113 <210> SEQ ID NO: 4
114 <211> LENGTH: 34
115 <212> TYPE: DNA
116 <213> ORGANISM: Artificial Sequence
118 <220> FEATURE:
119 <223> OTHER INFORMATION: Description of Artificial Sequence:FGF-CX Reverse
120     Primer
122 <400> SEQUENCE: 4
123 ctcgtcctcg agagtgtaca tcagtaggtc ctg 34
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127 <211> LENGTH: 424
128 <212> TYPE: DNA
129 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 5
132 tggatcattt aaaggggatt ctccaggcga ggcagctata ctgcaggact ggatttcact 60
133 tagaaatctt cccaatggt actatccagg gaaccaggaa agaccacagc cgatttggca 120
134 ttctggaatt tatcagtata gcagtgggce tggtcagcat tcgaggcgtg gacagtggac 180

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135 tctacctcgg gatgaatgag aaggggggagc tgtatggatc agaaaaacta acccaagagt 240
136 gtgtattcag agaacagttc gaagaaaact ggtataatac gtactcgtca aacctatata 300
137 agcacgtgga cactggaagg cgatactatg ttgcattaaa taaagatggg accccgagag 360
138 aagggactag gactaaacgg caccagaaat tcacacattt ttacctaga ccagtggacc 420
139 ccga 424

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143 &lt;211&gt; LENGTH: 288

144 &lt;212&gt; TYPE: DNA

145 &lt;213&gt; ORGANISM: Homo sapiens

147 &lt;400&gt; SEQUENCE: 6

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148 taccgaagag gctgtggtcc tgccgggtgc cctgcacgct gccgtcgggc aggatctgca 60
149 ggtggaagcc ggtgcggcaa tagagctgcc ggcgcgcagg atgccgtgca ggtgcgccag 120
150 ctgcgcagcc cccggcccgcc cgcgcgcgct ccgctccgcc gcgctcctgc gctcggccag 180
151 cagcggcggc cgctccccgg caggaggcaa caggaaatgc gaaccacact gctggcccaa 240
152 gccctccagg ccgccagaa agcccccgac ttgggctaag ggagccat 288

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155 &lt;210&gt; SEQ ID NO: 7

156 &lt;211&gt; LENGTH: 255

157 &lt;212&gt; TYPE: DNA

158 &lt;213&gt; ORGANISM: Homo sapiens

160 &lt;400&gt; SEQUENCE: 7

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161 agtgtacatc agtaggtcct tgtacaattc tggaactctt tctggatcca ctggtctagg 60
162 taagaaatgt gtaaatctct gatgcctctt ggacctggcg ccctctcttg gattccgtc 120
163 tttgttaagt gccacaaaat acctgcggcc agtgtctcca tgtttatata tgtagatga 180
164 ataggtgtta taccagttct ctccaaactg ctccctaaag atgcattcgg aagtaagttt 240
165 ctctgaaag agaga 255

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168 &lt;210&gt; SEQ ID NO: 8

169 &lt;211&gt; LENGTH: 106

170 &lt;212&gt; TYPE: DNA

171 &lt;213&gt; ORGANISM: Homo sapiens

173 &lt;400&gt; SEQUENCE: 8

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174 ctgatccata gagttctcct ttgtcattca ttccaagata gagaccactg tccacacctc 60
175 taatactgac cagtcacct gccacactga tgaattccaa gatacc 106

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178 &lt;210&gt; SEQ ID NO: 9

179 &lt;211&gt; LENGTH: 205

180 &lt;212&gt; TYPE: PRT

181 &lt;213&gt; ORGANISM: Homo sapiens

183 &lt;400&gt; SEQUENCE: 9

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184 Met Ala Pro Leu Gly Glu Val Gly Asn Tyr Phe Gly Val Gln Asp Ala
185   1           5           10           15
187 Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
188           20           25           30
190 Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
191           35           40           45
193 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
194           50           55           60
196 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
197           65           70           75           80
199 Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu
200           85           90           95

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202 Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
203           100           105           110
205 Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
206           115           120           125
208 Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
209           130           135           140
211 Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg
212 145           150           155           160
214 Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr
215           165           170           175
217 Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val
218           180           185           190
220 Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu
221           195           200           205

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224 &lt;210&gt; SEQ ID NO: 10

225 &lt;211&gt; LENGTH: 205

226 &lt;212&gt; TYPE: PRT

227 &lt;213&gt; ORGANISM: Mus musculus

229 &lt;400&gt; SEQUENCE: 10

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230 Met Ala Pro Leu Gly Glu Val Gly Ser Tyr Phe Gly Val Gln Asp Ala
231 1           5           10           15
233 Val Pro Phe Gly Asn Val Pro Val Leu Pro Val Asp Ser Pro Val Leu
234           20           25           30
236 Leu Asn Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
237           35           40           45
239 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
240           50           55           60
242 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
243 65           70           75           80
245 Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu
246           85           90           95
248 Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
249           100           105           110
251 Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
252           115           120           125
254 Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
255           130           135           140
257 Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg
258 145           150           155           160
260 Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr
261           165           170           175
263 Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val
264           180           185           190
266 Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu
267           195           200           205

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270 &lt;210&gt; SEQ ID NO: 11

271 &lt;211&gt; LENGTH: 205

272 &lt;212&gt; TYPE: PRT

273 &lt;213&gt; ORGANISM: Rattus norvegicus

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275 <400> SEQUENCE: 11
276 Met Ala Pro Leu Gly Glu Val Gly Ser Tyr Phe Gly Val Gln Asp Ala
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280           20           25           30
282 Leu Ser Asp His Leu Gly Gln Ser Glu Ala Gly Gly Leu Pro Arg Gly
283           35           40           45
285 Pro Ala Val Thr Asp Leu Asp His Leu Lys Gly Ile Leu Arg Arg Arg
286           50           55           60
288 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Glu Ile Phe Pro Asn Gly
289   65           70           75           80
291 Thr Ile Gln Gly Thr Arg Lys Asp His Ser Arg Phe Gly Ile Leu Glu
292           85           90           95
294 Phe Ile Ser Ile Ala Val Gly Leu Val Ser Ile Arg Gly Val Asp Ser
295           100          105          110
297 Gly Leu Tyr Leu Gly Met Asn Glu Lys Gly Glu Leu Tyr Gly Ser Glu
298           115          120          125
300 Lys Leu Thr Gln Glu Cys Val Phe Arg Glu Gln Phe Glu Glu Asn Trp
301           130          135          140
303 Tyr Asn Thr Tyr Ser Ser Asn Leu Tyr Lys His Val Asp Thr Gly Arg
304   145          150          155          160
306 Arg Tyr Tyr Val Ala Leu Asn Lys Asp Gly Thr Pro Arg Glu Gly Thr
307           165          170          175
309 Arg Thr Lys Arg His Gln Lys Phe Thr His Phe Leu Pro Arg Pro Val
310           180          185          190
312 Asp Pro Asp Lys Val Pro Glu Leu Tyr Lys Asp Ile Leu
313           195          200          205
316 <210> SEQ ID NO: 12
317 <211> LENGTH: 208
318 <212> TYPE: PRT
319 <213> ORGANISM: Xenopus laevis
321 <400> SEQUENCE: 12
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323   1           5           10           15
325 Leu Gly Gln Val Gly Ser His Phe Leu Leu Pro Pro Ala Lys Asp Ser
326           20           25           30
328 Pro Leu Leu Phe Asn Asp Pro Leu Ala Gln Ser Glu Arg Leu Ser Arg
329           35           40           45
331 Ser Ala Pro Ser Asp Leu Ser His Leu Gln Gly Ile Leu Arg Arg Arg
332           50           55           60
334 Gln Leu Tyr Cys Arg Thr Gly Phe His Leu Gln Ile Leu Pro Asp Gly
335   65           70           75           80
337 Asn Val Gln Gly Thr Arg Gln Asp His Ser Arg Phe Gly Ile Leu Glu
338           85           90           95
340 Phe Ile Ser Val Ala Ile Gly Leu Val Ser Ile Arg Gly Val Asp Thr
341           100          105          110
343 Gly Leu Tyr Leu Gly Met Asn Asp Lys Gly Glu Leu Phe Gly Ser Glu
344           115          120          125
346 Lys Leu Thr Ser Glu Cys Ile Phe Arg Glu Gln Phe Glu Glu Asn Trp

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/609,543

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